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MAINFRAME COMPUTER PROGRAMS FOR RAPID ANALYSIS OF  
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NAVAL BIOSCIENCES LAB A M NEUSCHATZ ET AL. 1985  
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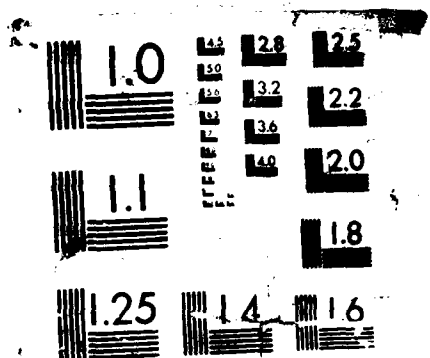
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MICROCOPY RESOLUTION TEST CHART

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ANDREW M. NEUSCHATZ,\* PAUL L. MILLER, & ALEXANDER E. KARU (Univ. of Calif. Naval Biosciences Laboratory, Oakland CA 94625) Mainframe Computer Programs for Rapid Analysis of Hybridoma Screening Data.

Most laboratories that currently produce large numbers of hybridomas grow them and screen their media by immunoassay in 96-well plates. Robotic systems are commercially available for sterile sampling, feeding, and expansion of hybridomas, and there are several semi-automated readers for 96-well immunoassay plates on the market. We have written a program package in Microsoft Pascal that converts the records from a Dynatech "Autoprep" automated hybridoma sampler and a Flow "Multiskan" enzyme immunoassay reader to an ASCII database format, merges them, and creates tables which can be sorted by any parameter (e.g., source plate/well, target plate/well, or assay result), and a histogram from which the best-responding hybridomas can be selected. Responses to multiple screening antigens can be merged into a single table for easy comparison. Separate directories are automatically set up for different experiments, allowing several data sets to be processed concurrently. Data may be input from any source as formatted flat ASCII files, and the package includes an option for transferring the tabulated data to other databases and MULTIFLAN spreadsheets. The package is menu-driven and very user-friendly, and it demonstrates a strategy for rapidly evaluating data for large numbers of hybridoma cultures. It was written on a Zilog System 8000 computer under UNIX, but may be ported to most micro- or minicomputers with a Pascal compiler and sufficient memory. This program package is copyrighted by the University of California. [supported by Contract N00014-81-C-0570 from the U.S. Office of Naval Research]

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